

SEQUENCE LISTING

<110> Abbott, Geoffrey W.
 Sesti, Federico
 Splawski, Igor
 Keating, Mark T.
 Goldstein, Steve A.N.
 University of Utah Research Foundation
 Yale University

<120> MinK-Related Genes, Formation of Potassium Channels and
 Association with Cardiac Arrhythmia

<130> KCNE2 et al.

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<150> US 60/129,404
 <151> 1999-04-15

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<170> PatentIn Ver. 2.0

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gac gtc ttc cga agg att ttt att act tat atg gac aat tgg cgc cag 157
 Asp Val Phe Arg Arg Ile Phe Ile Thr Tyr Met Asp Asn Trp Arg Gln
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aac aca aca gct gag caa gag gcc ctc caa gcc aaa gtt gat gct gag 205
 Asn Thr Thr Ala Glu Gln Glu Ala Leu Gln Ala Lys Val Asp Ala Glu
 30 35 40

aac ttc tac tat gtc atc ctg tac ctc atg gtg atg att gga atg ttc 253
 Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe
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 65 70 75

cgg gaa cac tcc aat gac ccc tac cac cag tac att gta gag gac tgg 349
 Arg Glu His Ser Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp
 80 85 90

cag gaa aag tac aag agc caa atc ttg aat cta gaa gaa tcg aag gcc 397
 Gln Glu Lys Tyr Lys Ser Gln Ile Leu Asn Leu Glu Glu Ser Lys Ala
 95 100 105

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 gatttatgct tgcttgttg agcaatattt tgtgctgaag acctctttta ctttccgggc 682
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 35 40 45
 Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ser Phe Ile Ile
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 Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
 65 70 75 80
 Asn Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Glu Lys Tyr
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aga gtg gat gcc gag aac ttc tac tac gtc atc ctg tac ctc atg gtg 199
 Arg Val Asp Ala Glu Asn Phe Tyr Tyr Val Ile Leu Tyr Leu Met Val
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 Met Ile Gly Met Phe Ala Phe Ile Val Val Ala Ile Leu Val Ser Thr
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gtg aag tcg aag cgg cgg gag cac tcc cag gac ccg tac cac cag tac 295
 Val Lys Ser Lys Arg Arg Glu His Ser Gln Asp Pro Tyr His Gln Tyr
 75 80 85

atc gtg gag gat tgg cag cag aag tat agg agt cag atc ttg cat ctg 343
 Ile Val Glu Asp Trp Gln Gln Lys Tyr Arg Ser Gln Ile Leu His Leu
 90 95 100

gaa gac tcc aag gcc acc atc cat gag aac ctg ggg gcg acg ggg ttc 391
 Glu Asp Ser Lys Ala Thr Ile His Glu Asn Leu Gly Ala Thr Gly Phe
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 35 40 45

Val Ile Leu Tyr Leu Met Val Met Ile Gly Met Phe Ala Phe Ile Val
 50 55 60

Val Ala Ile Leu Val Ser Thr Val Lys Ser Lys Arg Arg Glu His Ser
 65 70 75 80

Gln Asp Pro Tyr His Gln Tyr Ile Val Glu Asp Trp Gln Gln Lys Tyr
 85 90 95

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Pro Gly Pro Gly Leu Gly Pro Asp Asn Gln Thr Glu Glu Arg Arg Ala
      35          40          45
Ser Leu Pro Gly Arg Asp Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
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[illegible]

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aaggaactga ggggttgtgg gacatccacg aagagatcct caaagatgtc tcagagccag 180
cagagtctct gaactgtttg atcacattcc agctcttccc atacctcaat atctgttgct 240
atg gag act tcc aac ggg act gag acc tgg tac atg agc ctc cat gct 288
Met Glu Thr Ser Asn Gly Thr Glu Thr Trp Tyr Met Ser Leu His Ala
1 5 10 15
gtg ctg aag gct ctg aac aca acc ctt cac agt cac ttg ctc tgc cgg 336
Val Leu Lys Ala Leu Asn Thr Thr Leu His Ser His Leu Leu Cys Arg
20 25 30
cct ggg cca gga cca ggg cca gac aat caa act gag gat cgt cgg gct 384
Pro Gly Pro Gly Pro Gly Pro Asp Asn Gln Thr Glu Asp Arg Arg Ala
35 40 45
agc ctt cct ggt cgt aat gac aac tcc tac atg tat att ctc ttt gtc 432
Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
50 55 60
atg ttc cta ttt gcc gtc act gtg ggc agt ctc atc ctg gga tat acc 480
Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
65 70 75 80
cgt tca cgc aaa gtg gac aaa cgt agt gac ccc tat cat gtg tac atc 528
Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile
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aag aac cgt gtg tct atg atc tgatgtgagg aacctgaaga caatggaaga 579
Lys Asn Arg Val Ser Met Ile
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acagtgtatc tatgtaagat caacaggaaa ctggtaagag gattaggtca ttattaggac 699
cagagaagag ggactgatag gccagtcctt gtggatgaga catttttcga gacacagatg 759
cgcattataa actcagagcc catgaacaca tatatataaa gtatggacaa ccagcaagta 819

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 <212> PRT
 <213> Mus musculus

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 35 40 45
 Ser Leu Pro Gly Arg Asn Asp Asn Ser Tyr Met Tyr Ile Leu Phe Val
 50 55 60
 Met Phe Leu Phe Ala Val Thr Val Gly Ser Leu Ile Leu Gly Tyr Thr
 65 70 75 80
 Arg Ser Arg Lys Val Asp Lys Arg Ser Asp Pro Tyr His Val Tyr Ile
 85 90 95
 Lys Asn Arg Val Ser Met Ile
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (604)..(1113)

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 80 85 90 95
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 Ala Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser
 115 120 125
 gag tcc tcc tcc ccg gac gtg cac ctc acc att cag gag gag ggg gca 1032
 Glu Ser Ser Ser Pro Asp Val His Leu Thr Ile Gln Glu Glu Gly Ala
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<212> PRT
<213> Homo sapiens

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35 40 45
Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg Glu
50 55 60
Lys Lys Ser Ser Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu Trp
65 70 75 80
Gly Glu Ala Met Lys Pro Leu Pro Val Val Ser Gly Leu Arg Ser Val
85 90 95
Gln Val Pro Leu Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro Ala
100 105 110
Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser Glu
115 120 125
Ser Ser Ser Pro Asp Val His Leu Thr Ile Gln Glu Glu Gly Ala Asp
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Gly Ser Ser Glu Asn Ile His Gln Asn Ser
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<212> DNA
<213> Mus musculus

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Met Leu Arg Met Glu Pro Leu Asn Ser
1 5

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aaa gac gag gag agg ctg tgg ggg gag gct atg aag ccg cta cct atg 352
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 110 115 120

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 Pro Leu Asn Asp Ser Ser Glu Gly Ser Ser Glu Asn Ile His Gln Asn
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 gctgagttgt agacaattgt ctggtgtatt taatggttg taattttcac gatatttttt 2445
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 <213> Mus musculus

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 35 40 45
 Phe Leu Ile Gly Ile Met Leu Gly Tyr Met Lys Ser Lys Arg Arg Glu
 50 55 60
 Lys Lys Ser Ser Leu Leu Leu Tyr Lys Asp Glu Glu Arg Leu Trp
 65 70 75 80

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Gly Glu Ala Met Lys Pro Leu Pro Met Met Ser Gly Leu Arg Ser Gly
 85 90 95
 Gln Val Pro Met Met Leu Asn Met Leu Gln Glu Ser Val Ala Pro Ala
 100 105 110
 Leu Ser Cys Thr Leu Cys Ser Met Glu Gly Asp Ser Val Ser Ser Glu
 115 120 125
 Ser Ser Ser Pro Asp Val His Leu Pro Ile Gln Glu Glu Gly Ala Asp
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 145 150 155 160
 Gly Ser Ser Glu Asn Ile His Gln Asn Ser
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<210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer for
 mutation screening

<400> 13
 ccgttttcct aaccttggtc g

21

<210> 14
 <211> 21
 <212> DNA
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<220>
 <223> Description of Artificial Sequence:PCR primer for
 mutation screening

<400> 14
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21

<210> 15
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer for
 mutation screening

<400> 15
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23

<210> 16
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

004440"044400

<223> Description of Artificial Sequence:PCR primer for mutation screening

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<220>
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<220>
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<210> 19
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<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence:HA residues for epitope mapping

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<222> (10)
<223> Xaa represents encoded stop codon.

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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Xaa
1 5 10

<210> 20
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:cmv residues for epitope-mapping

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<222> (15)

004740" E9T0550

<223> Xaa represents encoded stop codon.

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